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SMART MODE:

NORMAL GENOMIC



Schultz et al. (1998) *Proc. Natl. Acad. Sci. USA* **95**, 5857-5864

Letunic et al. (2008) *Nucleic Acids Res* , doi:10.1093/nar/gkn808

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HTH_LUXR



helix_turn_helix, Lux Regulon

SMART

accession SM00421
number:

Description: lux regulon (activates the bioluminescence operon)

This domain is a DNA-binding, helix-turn-helix (HTH) domain of about 65 amino acids, present in transcription regulators of the LuxR/FixJ family of response regulators. The domain is named after *Vibrio fischeri* luxR, a transcriptional activator for quorum-sensing control of luminescence. LuxR-type HTH domain proteins occur in a variety of organisms. The DNA-binding HTH domain is usually located in the C-terminal region; the N-terminal region often containing an autoinducer-binding domain or a response regulatory domain. Most luxR-type regulators act as transcription activators, but some can be repressors or have a dual role for different sites. LuxR-type HTH regulators control a wide variety of activities in various biological processes.

The luxR-type, DNA-binding HTH domain forms a four-helical bundle structure. The HTH motif comprises the second and third helices, known as the scaffold and recognition helix, respectively. The HTH binds DNA in the major groove, where the N-terminal part of the recognition helix makes most of the DNA contacts. The fourth helix is involved in dimerisation of gerE and traR. Signalling events by one of the four activation mechanisms described below lead to multimerisation of the regulator. The

regulators bind DNA as multimers ([PUBMED:11243786](#)), ([PUBMED:12740396](#)), ([PUBMED:12087407](#)).

LuxR-type HTH proteins can be activated by one of four different mechanisms:

1) Regulators which belong to a two-component sensory transduction system where the protein is activated by its phosphorylation, generally on an aspartate residue, by a transmembrane kinase ([PUBMED:12352954](#)), ([PUBMED:12162958](#)). Some proteins that belong to this category are:

- Rhizobiaceae fixJ (global regulator inducing expression of nitrogen-fixation genes in microaerobiosis)
- *Escherichia coli* and *Salmonella typhimurium* uhpA (activates hexose phosphate transport gene uhpT)
- *E. coli* narL and narP (activate nitrate reductase operon)
- Enterobacteria rcsB (regulation of exopolysaccharide biosynthesis in enteric and plant pathogenesis)
- *Bordetella pertussis* bvgA (virulence factor)
- *Bacillus subtilis* coma (involved in expression of late-expressing competence genes)

**Interpro
abstract
(IPR000792):**

2) Regulators which are activated, or in very rare cases repressed, when bound to N-acyl homoserine lactones, which are used as quorum sensing molecules in a variety of Gram-negative bacteria ([PUBMED:15255890](#)):

- *V. fischeri* luxR (activates bioluminescence operon)
- *Agrobacterium tumefaciens* traR (regulation of Ti plasmid transfer)
- *Erwinia carotovora* carR (control of carbapenem antibiotics biosynthesis)
- *E. carotovora* expR (virulence factor for soft rot disease; activates plant tissue macerating enzyme genes)
- *Pseudomonas aeruginosa* lasR (activates elastase gene lasB)
- *Erwinia chrysanthemi* echR and *Erwinia stewartii* esaR
- *Pseudomonas chlororaphis* phzR (positive regulator of phenazine antibiotic production)
- *Pseudomonas aeruginosa* rhIR (activates rhlAB operon and lasB gene)

3) Autonomous effector domain regulators, without a regulatory domain, represented by gerE ([PUBMED:11243786](#)).

- *B. subtilis* gerE (transcription activator and repressor for the regulation of spore formation)

4) Multiple ligand-binding regulators, exemplified by malT ([PUBMED:11931562](#)).

- *E. coli* malT (activates maltose operon; MalT binds ATP and maltotriose)

GO process: regulation of transcription, DNA-dependent ([GO:0006355](#))

GO component: intracellular ([GO:0005622](#))

GO function: transcription factor activity ([GO:0003700](#)), sequence-specific DNA binding ([GO:0043565](#))

Family alignment: View [Alignment consensus sequence](#) or [Family alignment in CHROMA format](#)

There are [6090](#) HTH_LUXR domains in 6082 proteins in [SMART's nrdb](#) database.

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